

10/586229

WO 2005/116076

PCT/IB2005/002480

1/21

AP20 Rec'd PCT/PTO 19 JUL 2006

SEQUENCE LISTING

F

<110> OncoMab GmbH et al.

<120> Neoplasm-Specific Polypeptides and Their
Uses

<130> 50308/009W03

<150> 10/764,730

<151> 2004-01-26

<160> 30

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 288

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(288)

<400> 1

tcc tgc aag gct tct ggc tac acc ttc act gac tac tat ata aac tgg 48
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp
1 5 10 15

gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag att tat 96
Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
20 25 30

cct gga agt ggt aat act tac tac aat gag aag ttc aag ggc aag gcc 144
Pro Gly Ser Gly Asn Thr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
35 40 45

aca ctg act gca gac aaa tcc tcc agc aca gcc tac atg cag ctc agc 192
Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met Gln Leu Ser
50 55 60

agc ctg aca tct gag gac tct gca gtc tat ttc tgt gca aga tcg gga 240
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
65 70 75 80

tta cga ccc tat gct atg gac tac tgg ggt caa gga acc tca gtc acc 288
Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
85 90 95

<210> 2

<211> 96

<212> PRT

<213> Mus musculus

<400> 2

Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Tyr	Ile	Asn	Trp
1						5			10					15	
Val	Lys	Gln	Arg	Thr	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Glu	Ile	Tyr
								20	25				30		
Pro	Gly	Ser	Gly	Asn	Thr	Tyr	Tyr	Asn	Glu	Lys	Phe	Lys	Gly	Lys	Ala
								35	40			45			
Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	Gln	Leu	Ser
								50	55		60				
Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Ser	Gly
	65			70					75			80			
Leu	Arg	Pro	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr
					85				90			95			

<210> 3

<211> 315

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(315)

<400> 3

cca	ctc	tcc	ctg	cct	gtc	agt	ctt	gga	gat	caa	gcc	tcc	atc	tct	tgc
Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys
1								10					15		

aga	tct	agt	cag	agc	att	gta	cat	agt	aat	gga	aac	acc	tat	tta	gaa
Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu
					20			25				30			

tgg	tac	ctg	cag	aaa	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	tac	aaa
Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys
					35			40				45			

gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	gga
Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly
					50			55		60					

tca	ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	gag	gat
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp
					65			70		75		80			

ctg	gga	gtt	tat	tac	tgc	ttt	caa	ggt	tca	cat	gtt	ccg	tac	acg	ttc
Leu	Gly	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Tyr	Thr	Phe
					85			90			95				

gga	ggg	ggg	acc	aag	ctg	gaa	ata	aaa							315
Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys							
					100			105							

<210> 4

<211> 105

<212> PRT

<213> Mus musculus

<400> 4

Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	
1								10						15		
Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Tyr	Leu	Glu
					20			25						30		
Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	
					35			40						45		
Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	
					50			55			60					
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	
					65			70			75			80		
Leu	Gly	Val	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Tyr	Thr	Phe	
					85			90						95		
Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	.							
					100			105								

<210> 5

<211> 3114

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(3114)

<400> 5

gat	gtg	agg	gag	cct	gaa	aat	gaa	att	tct	tca	gac	tgc	aat	cat	ttg
Asp	Val	Arg	Glu	Pro	Glu	Asn	Glu	Ile	Ser	Ser	Asp	Cys	Asn	His	Leu
1								10						15	

ttg	tgg	aat	tat	aag	ctg	aac	cta	act	aca	gat	ccc	aaa	ttt	gaa	tct
Leu	Trp	Asn	Tyr	Lys	Leu	Asn	Leu	Thr	Thr	Asp	Pro	Lys	Phe	Glu	Ser
					20			25					30		

gtg	gcc	aga	gag	gtt	tgc	aaa	tct	act	ata	aca	gag	att	gaa	gaa	tgt
Val	Ala	Arg	Glu	Val	Cys	Lys	Ser	Thr	Ile	Thr	Glu	Ile	Glu	Glu	Cys
					35			40					45		

gct	gat	gaa	ccg	gtt	gga	aaa	ggt	tac	atg	gtt	tcc	tgc	ttg	gtg	gat
Ala	Asp	Glu	Pro	Val	Gly	Lys	Gly	Tyr	Met	Val	Ser	Cys	Leu	Val	Asp
					50			55					60		

cac	cga	ggc	aac	atc	act	gag	tat	cag	tgt	cac	cag	tac	att	acc	aag
His	Arg	Gly	Asn	Ile	Thr	Glu	Tyr	Gln	Cys	His	Gln	Tyr	Ile	Thr	Lys
					65			70					80		

atg	acg	gcc	atc	att	ttt	agt	gat	tac	cgt	tta	atc	tgt	ggc	ttc	atg
Met	Thr	Ala	Ile	Ile	Phe	Ser	Asp	Tyr	Arg	Leu	Ile	Cys	Gly	Phe	Met
					85			90					95		

gat	gac	tgc	aaa	aat	gac	atc	aac	att	ctg	aaa	tgt	ggc	agt	att	cgg
Asp	Asp	Cys	Lys	Asn	Asp	Ile	Asn	Ile	Leu	Lys	Cys	Gly	Ser	Ile	Arg
					100			105					110		

ctt gga gaa aag gat gca cat tca caa ggt gag gtg gta tca tgc ttg			384
Leu Gly Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu			
115	120	125	
· gag aaa ggc ctg gtg aaa gaa gca gaa gaa aga gaa ccc aag att caa			432
Glu Lys Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln			
130	135	140	
gtt tct gaa ctc tgc aag aaa gcc att ctc cggt gct gag ctg tca			480
Val Ser Glu Leu Cys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser			
145	150	155	160
tcg gat gac ttt cac tta gac cggt cat tta tat ttt gct tgc cga gat			528
Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp			
165	170	175	
gat cgg gag cgt ttt tgt gaa aat aca caa gct ggt gag ggc aga gtg			576
Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val			
180	185	190	
tat aag tgc ctc ttt aac cat aaa ttt gaa gaa tcc atg agt gaa aag			624
Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys			
195	200	205	
tgt cga gaa gca ctt aca acc cgc caa aag ctg att gcc cag gat tat			672
Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr			
210	215	220	
aaa gtc agt tat tca ttg gcc aaa tcc tgt aaa agt gac ttg aag aaa			720
Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys			
225	230	235	240
tac cgg tgc aat gtg gaa aac ctt ccgt cga tcg cgt gaa gcc agg ctc			768
Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu			
245	250	255	
tcc tac ttg tta atg tgc ctg gag tca gct gta cac aga ggg cga caa			816
Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln			
260	265	270	
gtc agc agt gag tgc cag ggg gag atg ctg gat tac cga cgc atg ttg			864
Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu			
275	280	285	
atg gaa gac ttt tct ctg agc cct gag atc atc cta agc tgt cgg ggg			912
Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly			
290	295	300	
gag att gaa cac cat tgt tcc gga tta cat cga aaa ggg cgg acc cta			960
Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu			
305	310	315	320
cac tgt ctg atg aaa gta gtt cga ggg gag aag ggg aac ctt gga atg			1008
His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met			
325	330	335	

aac tgc cag cag gcg ctt caa aca ctg att cag gag act gac cct ggt Asn Cys Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly	340	345	350	1056
gca gat tac cgc att gat cga gct ttg aat gaa gct tgt gaa tct gta Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val	355	360	365	1104
atc cag aca gcc tgc aaa cat ata aga tct gga gac cca atg atc ttg Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu	370	375	380	1152
tcg tgc ctg atg gaa cat tta tac aca gag aag atg gta gaa gac tgt Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys	385	390	395	1200
gaa cac cgt ctc tta gag ctg cag tat ttc atc tcc cgg gat tgg aag Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys	405	410	415	1248
ctg gac cct gtc ctg tac cgc aag tgc cag gga gac gct tct cgt ctt Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu	420	425	430	1296
tgc cac acc cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly	435	440	445	1344
gct gtg ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln	450	455	460	1392
gga agg agg ctc tca cgg gag tgc cga gct gaa gtc caa agg atc cta Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu	465	470	475	1440
cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat aag His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys	485	490	495	1488
tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag act gga Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly	500	505	510	1536
cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta gtg gtg gag Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu	515	520	525	1584
tgt aga gat ata gtt ggc aac ctc act gag tta gaa tca gag gat att Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile	530	535	540	1632
caa ata gaa gcc ttg ctg atg aga gcc tgt gag ccc ata att cag aac Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn	545	550	555	1680
ttc tgc cac gat gtg gca gat aac cag ata gac tcc ggg gac ctg atg				1728

Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met			
565	570	575	
gag tgt ctg ata cag aac aaa cac cag aag gac atg aac gag aag tgt 1776			
Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys			
580	585	590	
gcc atc gga gtt acc cac ttc cag ctg gtg cag atg aag gat ttt cg 1824			
Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg			
595	600	605	
ttt tct tac aag ttt aaa atg gcc tgc aag gag gac gtg ttg aag ctt 1872			
Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu			
610	615	620	
tgc cca aac ata aaa aag aag gtg gac gtg gtg atc tgc ctg agc acg 1920			
Cys Pro Asn Ile Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr			
625	630	635	640
acc gtg cgc aat gac act ctg cag gaa gcc aag gag cac agg gtg tcc 1968			
Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser			
645	650	655	
ctg aag tgc cgc agg cag ctc cgt gtg gag gag ctg gag atg acg gag 2016			
Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu			
660	665	670	
gac atc cgc ttg gag cca gat cta tac gaa gcc tgc aag agt gac atc 2064			
Asp Ile Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile			
675	680	685	
aaa aac ttc tgt tcc gct gtg caa tat ggc aac gct cag att atc gaa 2112			
Lys Asn Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu			
690	695	700	
tgt ctg aaa gaa aac aag aag cag cta agc acc cgc tgc cac caa aaa 2160			
Cys Leu Lys Glu Asn Lys Gln Leu Ser Thr Arg Cys His Gln Lys			
705	710	715	720
gta ttt aag ctg cag gag aca gag atg atg gac cca gag cta gac tac 2208			
Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr			
725	730	735	
acc ctc atg agg gtc tgc aag cag atg ata aag aag ttc tgt ccg gaa 2256			
Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys Pro Glu			
740	745	750	
gca gat tct aaa acc atg ttg cag tgc ttg aag caa aat aaa aac agt 2304			
Ala Asp Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser			
755	760	765	
gaa ttg atg gat ccc aaa tgc aaa cag atg ata acc aag cgc cag atc 2352			
Glu Leu Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile			
770	775	780	
acc cag aac aca gat tac cgc tta aac ccc atg tta aga aaa gcc tgt 2400			
Thr Gln Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys			

7/21

785	790	795	800	
aaa gct gac att cct aaa ttc tgt cac ggt atc ctg act aag gcc aag Lys Ala Asp Ile Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys 805	810	815		2448
gat gat tca gaa tta gaa gga caa gtc atc tct tgc ctg aag ctg aga Asp Asp Ser Glu Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg 820	825	830		2496
tat gct gac cag cgc ctg tct tca gac tgt gaa gac cag atc cga atc Tyr Ala Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile 835	840	845		2544
att atc cag gag tcc gcc ctg gac tac cgc ctg gat cct cag ctc cag Ile Ile Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln 850	855	860		2592
ctg cac tgc tca gac gag atc tcc agt cta tgt gct gaa gaa gca gca Leu His Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala 865	870	875	880	2640
gcc caa gag cag aca ggt cag gtg gag gag tgc ctc aag gtc aac ctg Ala Gln Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu 885	890	895		2688
ctc aag atc aaa aca gaa ttg tgt aaa aag gaa gtg cta aac atg ctg Leu Lys Ile Lys Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu 900	905	910		2736
aag gaa agc aaa gca gac atc ttt gtt gac ccg gta ctt cat act gct Lys Glu Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala 915	920	925		2784
tgt gcc ctg gac att aaa cac cac tgc gca gcc atc acc cct ggc cgc Cys Ala Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg 930	935	940		2832
ggg cgt caa atg tcc tgt ctc atg gaa gca ctg gag gat aag cgg gtg Gly Arg Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val 945	950	955	960	2880
agg tta cag ccc gag tgc aaa aag cgc ctc aat gac cgg att gag atg Arg Leu Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met 965	970	975		2928
tgg agt tac gca gca aag gtg gcc cca gca gat ggc ttc tct gat ctt Trp Ser Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu 980	985	990		2976
gcc atg caa gta atg acg tct cca tct aag aac tac att ctc tct gtg Ala Met Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val 995	1000	1005		3024
atc agt ggg agc atc tgt ata ttg ttc ctg att ggc ctg atg tgt gga Ile Ser Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly 1010	1015	1020		3072

cgg atc acc aag cga gtg aca cga gag ctc aag gac agg tag 3114
 Arg Ile Thr Lys Arg Val Thr Arg Glu Leu Lys Asp Arg *

1025	1030	1035
------	------	------

<210> 6
<211> 1037
<212> PRT
<213> Homo sapiens

<400> 6
 Asp Val Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu
 1 5 10 15
 Leu Trp Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser
 20 25 30
 Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Glu Glu Cys
 35 40 45
 Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp
 50 55 60
 His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys
 65 70 75 80
 Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met
 85 90 95
 Asp Asp Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg
 100 105 110
 Leu Gly Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu
 115 120 125
 Glu Lys Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln
 130 135 140
 Val Ser Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser
 145 150 155 160
 Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp
 165 170 175
 Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val
 180 185 190
 Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys
 195 200 205
 Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr
 210 215 220
 Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys
 225 230 235 240
 Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu
 245 250 255
 Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln
 260 265 270
 Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu
 275 280 285
 Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly
 290 295 300
 Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu
 305 310 315 320
 His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met
 325 330 335
 Asn Cys Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly
 340 345 350

Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val
355 360 365
Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu
370 375 380
Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys
385 390 395 400
Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys
405 410 415
Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu
420 425 430
Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly
435 440 445
Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln
450 455 460
Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu
465 470 475 480
His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys
485 490 495
Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly
500 505 510
Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu
515 520 525
Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile
530 535 540
Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn
545 550 555 560
Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met
565 570 575
Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys
580 585 590
Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg
595 600 605
Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu
610 615 620
Cys Pro Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr
625 630 635 640
Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser
645 650 655
Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu
660 665 670
Asp Ile Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile
675 680 685
Lys Asn Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu
690 695 700
Cys Leu Lys Glu Asn Lys Gln Leu Ser Thr Arg Cys His Gln Lys
705 710 715 720
Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr
725 730 735
Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys Pro Glu
740 745 750
Ala Asp Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser
755 760 765
Glu Leu Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile
770 775 780
Thr Gln Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys
785 790 795 800
Lys Ala Asp Ile Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys

10/21

805	810	815
Asp Asp Ser Glu Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg		
820	825	830
Tyr Ala Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile		
835	840	845
Ile Ile Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln		
850	855	860
Leu His Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala		
865	870	875
Ala Gln Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu		
885	890	895
Leu Lys Ile Lys Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu		
900	905	910
Lys Glu Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala		
915	920	925
Cys Ala Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg		
930	935	940
Gly Arg Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val		
945	950	955
Arg Leu Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met		
965	970	975
Trp Ser Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu		
980	985	990
Ala Met Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val		
995	1000	1005
Ile Ser Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly		
1010	1015	1020
Arg Ile Thr Lys Arg Val Thr Arg Glu Leu Lys Asp Arg		
1025	1030	1035

<210> 7
<211> 1177
<212> PRT
<213> Homo sapiens

<400> 7		
Met Ala Ala Cys Gly Arg Val Arg Arg Met Phe Arg Leu Ser Ala Ala		
1	5	10
Leu His Leu Leu Leu Phe Ala Ala Gly Gly Arg Asn Ser Pro Ala		
20	25	30
Arg Ala Ser His Ser Gln Gly Gln Gly Pro Gly Ala Asn Phe Val Ser		
35	40	45
Phe Val Gly Gln Ala Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro		
50	55	60
Gln Leu Pro Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln		
65	70	75
Gln Gln Gln Pro Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly		
85	90	95
Pro Pro Arg Arg Gly Gly Ala Gly Gly Gly Trp Lys Leu Ala		
100	105	110
Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys His		
115	120	125
Thr Trp Ser Asn Asn Leu Ala Val Leu Glu Cys Leu Gln Asp Val Arg		
130	135	140
Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu Leu Trp Asn		
145	150	155
		160

Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser Val Ala Arg
165 170 175
Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Lys Glu Cys Ala Asp Glu
180 185 190
Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp His Arg Gly
195 200 205
Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys Met Thr Ala
210 215 220
Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met Asp Asp Cys
225 230 235 240
Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg Leu Gly Glu
245 250 255
Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu Glu Lys Gly
260 265 270
Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser Glu
275 280 285
Leu Cys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser Ser Asp Asp
290 295 300
Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp Asp Arg Glu
305 310 315 320
Arg Phe Cys Glu Asn Thr Gln Ala Cys Glu Gly Arg Val Tyr Lys Cys
325 330 335
Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys Cys Arg Glu
340 345 350
Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr Lys Val Ser
355 360 365
Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys Tyr Arg Cys
370 375 380
Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu Ser Tyr Leu
385 390 395 400
Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln Val Ser Ser
405 410 415
Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu Met Glu Asp
420 425 430
Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly Glu Ile Glu
435 440 445
His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu His Cys Leu
450 455 460
Met Lys Val Val Arg Gly Glu Lys Cys Asn Leu Gly Met Asn Cys Gln
465 470 475 480
Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly Ala Asp Tyr
485 490 495
Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val Ile Gln Thr
500 505 510
Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Ser Ser Cys Leu
515 520 525
Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys Glu His Arg
530 535 540
Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys Leu Asp Pro
545 550 555 560
Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu Cys His Thr
565 570 575
His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly Ala Val Phe
580 585 590
Ser Cys Leu Tyr Arg Glu Ala Tyr Arg Thr Glu Glu Gln Gly Arg Arg
595 600 605
Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu His Gln Arg

12/21

610	615	620
Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys Cys Leu Ile		
625	630	635
Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly Gln Glu Leu		640
645	650	655
Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu Cys Arg Asp		
660	665	670
Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile Gln Ile Glu		
675	680	685
Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Thr Phe Cys His		
690	695	700
Asp Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met Glu Cys Leu Ile		
705	710	715
Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys Ala Ile Gly Val		720
725	730	735
Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg Phe Ser Tyr Lys		
740	745	750
Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro Asn Ile		
755	760	765
Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val Arg Asn		
770	775	780
Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys Cys Arg		
785	790	795
Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile Arg Leu		800
805	810	815
Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn Phe Cys		
820	825	830
Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys Leu Lys Glu		
835	840	845
Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys Val Phe Lys Leu		
850	855	860
Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr Thr Leu Met Arg		
865	870	875
Val Cys Lys Gln Met Ile Lys Arg Phe Cys Pro Glu Ala Asp Ser Lys		880
885	890	895
Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser Glu Leu Met Asp		
900	905	910
Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile Thr Gln Asn Thr		
915	920	925
Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys Lys Ala Asp Ile		
930	935	940
Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys Asp Asp Ser Glu		
945	950	955
Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg Tyr Ala Asp Gln		960
965	970	975
Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile Gln Glu		
980	985	990
Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His Cys Ser		
995	1000	1005
Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln Glu Gln		
1010	1015	1020
Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys Ile Lys		
1025	1030	1035
Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu Ser Lys		1040
1045	1050	1055
Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala Leu Asp		
1060	1065	1070

Ile Lys His His Cys Ala Ala Leu Thr Pro Gly Arg Gly Arg Gln Met
 1075 1080 1085
 Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val Arg Leu Gln Pro
 1090 1095 1100
 Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met Trp Ser Tyr Ala
 1105 1110 1115 1120
 Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu Ala Met Gln Val
 1125 1130 1135
 Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val Ile Ser Gly Ser
 1140 1145 1150
 Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly Arg Ile Thr Lys
 1155 1160 1165
 Arg Val Thr Arg Glu Leu Lys Asp Arg
 1170 1175

<210> 8
<211> 1179
<212> PRT
<213> Homo sapiens

<400> 8
 Met Ala Ala Cys Gly Arg Val Arg Arg Met Phe Arg Leu Ser Ala Ala
 1 5 10 15
 Leu His Leu Leu Leu Phe Ala Ala Gly Ala Glu Lys Leu Pro Gly
 20 25 30
 His Gly Val His Ser Gln Gly Gln Gly Pro Gly Ala Asn Phe Val Ser
 35 40 45
 Phe Val Gly Gln Ala Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro
 50 55 60
 Gln Leu Leu Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Gln Gln Gln Leu Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly
 85 90 95
 Pro Pro Ala Arg Arg Gly Gly Ala Gly Gly Gly Trp Lys Leu
 100 105 110
 Ala Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys
 115 120 125
 His Thr Trp Ser Asn Asn Leu Ala Val Leu Glu Cys Leu Gln Asp Val
 130 135 140
 Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu Leu Trp
 145 150 155 160
 Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser Val Ala
 165 170 175
 Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Lys Glu Cys Ala Asp
 180 185 190
 Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp His Arg
 195 200 205
 Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys Met Thr
 210 215 220
 Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met Asp Asp
 225 230 235 240
 Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg Leu Gly
 245 250 255
 Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu Glu Lys
 260 265 270
 Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser

275	280	285
Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu	Leu Ser Ser Asp	
290	295	300
Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys	Arg Asp Asp Arg	
305	310	315
Glu Arg Phe Cys Glu Asn Thr Gln Ala Arg Glu	Gly Arg Val Tyr Lys	
325	330	335
Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser	Glu Lys Cys Arg	
340	345	350
Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln	Asp Tyr Lys Val	
355	360	365
Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp	Leu Lys Tyr Arg	
370	375	380
Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu	Ala Arg Leu Ser Tyr	
385	390	395
Leu Leu Met Cys Leu Glu Ser Ala Val His Arg	Gly Arg Gln Val Ser	
405	410	415
Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg	Arg Met Leu Met Glu	
420	425	430
Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys	Arg Gly Glu Ile	
435	440	445
Glu His His Cys Ser Gly Leu His Arg Lys Gly	Arg Thr Leu His Cys	
450	455	460
Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn	Leu Gly Met Asn Cys	
465	470	475
Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu	Thr Asp Pro Gly Ala Asp	
485	490	495
Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys	Glu Ser Val Ile Gln	
500	505	510
Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro	Met Ile Leu Ser Cys	
515	520	525
Leu Met Glu His Leu Tyr Thr Glu Lys Met Val	Glu Asp Cys Glu His	
530	535	540
Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg	Asp Trp Lys Leu Asp	
545	550	555
Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp	Ala Ser Arg Leu Cys His	
565	570	575
Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met	Pro Gln Gly Ala Val	
580	585	590
Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg	Thr Glu Glu Gln Gly Arg	
595	600	605
Arg Leu Leu Asp Pro Ala Leu Gln Asp Lys Cys	Leu Ile Asp Leu Gly	
610	615	620
Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly	Gln Glu Leu Glu Cys Leu	
625	630	635
Ser Arg Glu Cys Arg Ala Glu Val Gln Arg	Ile Leu His Gln Arg Ala	
645	650	655
Met Asp Val Lys Gln Asp His Leu Asp Asp	Leu Val Val Glu Cys Arg	
660	665	670
Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser	Glu Asp Ile Gln Ile	
675	680	685
Glu Ala Leu Leu Met Arg Ala Cys Glu Pro	Ile Ile Gln Asn Phe Cys	
690	695	700
His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly	Asp Leu Met Glu Cys	
705	710	715
Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn	Glu Lys Cys Ala Ile	
725	730	735

Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg Phe Ser
 740 745 750
 Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro
 755 760 765
 Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val
 770 775 780
 Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys
 785 790 795 800
 Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile
 805 810 815
 Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn
 820 825 830
 Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys Leu
 835 840 845
 Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys Val Phe
 850 855 860
 Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr Thr Leu
 865 870 875 880
 Met Arg Val Cys Lys Gln Met Ile Lys Arg Phe Cys Pro Glu Ala Asp
 885 890 895
 Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser Glu Leu
 900 905 910
 Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile Thr Gln
 915 920 925
 Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys Lys Ala
 930 935 940
 Asp Ile Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys Asp Asp
 945 950 955 960
 Ser Glu Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg Tyr Ala
 965 970 975
 Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile
 980 985 990
 Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His
 995 1000 1005
 Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln
 1010 1015 1020
 Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys
 1025 1030 1035 1040
 Ile Lys Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu
 1045 1050 1055
 Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala
 1060 1065 1070
 Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg Gly Arg
 1075 1080 1085
 Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val Arg Leu
 1090 1095 1100
 Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met Trp Ser
 1105 1110 1115 1120
 Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu Ala Met
 1125 1130 1135
 Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val Ile Ser
 1140 1145 1150
 Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly Arg Ile
 1155 1160 1165
 Thr Lys Arg Val Thr Arg Glu Leu Lys Asp Arg
 1170 1175

<210> 9
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gcttggagaa aggcctggtg aa 22

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
tggcacttgc ggtacaggac ag 22

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gcagcttcag cagcaacagc a 21

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
cagctcagcc acccggagaa tg 22

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
gcttggagaa aggcctggtg aa 22

<210> 14

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
tggcacttgc ggtacaggac ag 22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gaacaccgtc tcttagagct gc 22

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gcttcctgca gagtgtaattt gc 22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
ggaggacgtg ttgaagcttt gc 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
ccagggcaca agcagtatga ag 22

<210> 19
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 19

caacagcaga caggtcaggt gg

22

<210> 20

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 20

ccggaaggtc tgggtatg ag

22

<210> 21

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

attnaacctt cactaaaggg

20

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

gtaatacgac tcactatagg gc

22

<210> 23

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 23

ccggaaggtc tgggtatg ag

22

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gtgaaaggac tcatgaccac agtc 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
catgtgggcc atgaggtcca ccac 24

<210> 26
<211> 312
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (312)
<223>

<400> 26
agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc 48
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
1 5 10 15

tat ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg 96
Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
20 25 30

gtg gca gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc 144
Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser
35 40 45

gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg 192
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
50 55 60

tat ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac 240
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
65 70 75 80

tgt gcg agg tcg act acg agg tct tat cct cta tac ggt atg gac gtt 288
Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro Leu Tyr Gly Met Asp Val
85 90 95

tgg ggc caa ggg aac cct gtc acc 312
Trp Gly Gln Gly Asn Pro Val Thr
100

<210> 27
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) . . . (399)
<223>

<400> 27

gtg acc tcc tat gtg ctg act cag cca ccc tcg gtg tca gtg gcc cca	48
Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro	
1 5 10 15	

gga cag acg gcc agt att acc tgt ggg gga aat aac att gga agt aaa	96
Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys	
20 25 30	

agt gtg cac tgg tac cat cag aag cca ggc cag gcc cct gtg ctg gtc	144
Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val	
35 40 45	

gtc tat gat gat agc gac cg ^g ccc tca ggg atc cct gag cga ttc tct	192
Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser	
50 55 60	

ggc tcc aac tct ggg aac acg gcc acc ctg acc atc acc agg gtc gaa	240
Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu	
65 70 75 80	

gcc ggg gat gag gcc gac tat tac tgt cag gtg tgg gat agt agt agt	288
Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser	
85 90 95	

gat ctc aat tgg gtg ttc ggc gga agg acc caa gct gac cgt cct acg	336
Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr	
100 105 110	

tca gcc caa ggc tgc ccc tcc ggt cac tct gtt ccc cgc ccc cct ctg	384
Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu	
115 120 125	

aag agc ttc aag ctt	399
Lys Ser Phe Lys Leu	
130	

<210> 28
<211> 104
<212> PRT
<213> Homo sapiens

<400> 28

Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser	
1 5 10 15	
Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp	

20 25 30
Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser
35 40 45
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
50 55 60
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
65 70 75 80
Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro Leu Tyr Gly Met Asp Val
85 90 95
Trp Gly Gln Gly Asn Pro Val Thr
100

<210> 29

<211> 133

<212> PRT

<213> Homo sapiens

<400> 29

Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro
1 5 10 15
Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys
20 25 30
Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val
35 40 45
Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser
50 55 60
Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu
65 70 75 80
Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser
85 90 95
Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr
100 105 110
Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu
115 120 125
Lys Ser Phe Lys Leu
130

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30

caagagcaga caggtcaggt gg